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Jaime L. Patera

*University of Nebraska - Lincoln*

Jennifer C. Copeland

*University of Nebraska-Lincoln*

Alexander Eletsy

*The State University of New York at Buffalo*

Greg A. Somerville

*University of Nebraska-Lincoln, gsomerville3@unl.edu*

Thomas Szyperski

*State University of New York at Buffalo*

*See next page for additional authors*

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**Authors**

Jaime L. Patera, Jennifer C. Copeland, Alexander Eletsy, Greg A. Somerville, Thomas Szyperski, and Robert Powers

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## Identification of low molecular weight compounds inhibiting growth of Corynebacteria: potential lead compounds for antibiotics

Dr. Jaime L. Stark<sup>[a]</sup>, Dr. Jennifer C. Copeland<sup>[a]</sup>, Dr. Alexander Eletsy<sup>[b]</sup>, Prof. Greg A. Somerville<sup>[c]</sup>, Prof. Thomas Szyperski<sup>[b]</sup>, and Prof. Robert Powers<sup>\*,[a]</sup>

<sup>[a]</sup>Department of Chemistry University of Nebraska-Lincoln Lincoln, NE, 68588-0304

<sup>[b]</sup>Department of Chemistry The State University of New York at Buffalo Buffalo, NY 14260

<sup>[c]</sup>School of Veterinary Medicine and Biomedical Sciences University of Nebraska-Lincoln Lincoln, NE, 68588-0905

### Keywords

Antibiotics; Corynebacteria; Drug Discovery; FAST-NMR; NMR Spectroscopy

The genus *Corynebacterium* consists of nearly seventy species and is closely related to the genera *Mycobacterium*, *Nocardia*, and *Rhodococcus*. The characteristic traits of Corynebacteria include cells that are shaped like straight rods with clubbed ends, as well as an extra cell wall layer consisting of mycolic acids covalently bound to the peptidoglycan layer which adds an additional layer of protection against antibiotics. Corynebacteria are very well studied and outstandingly important for the large scale biotechnological production of amino acids and nucleotides.<sup>[1]</sup> Moreover, Corynebacteria produce several pathogens that affect humans and livestock. Toxins produced by *C. diphtheriae* and *C. ulcerans* cause diphtheria, a highly contagious respiratory infection in humans,<sup>[2]</sup> or diphtheria-like symptoms,<sup>[2–3]</sup> respectively. *C. pseudotuberculosis* causes “cheesy gland” disease in goats and sheep resulting in significant economic losses.<sup>[2, 4]</sup> Moreover, while rare, many other Corynebacteria species have also been shown to cause infections. Therefore, elucidating the functional roles of uncharacterized proteins from Corynebacteria is of high biomedical and economic importance.

Protein CG2496 from *Corynebacterium glutamicum* (UniProtKB ID: Q6M3G5, Q8NNC9; Gene ID: CG2496, Cgl2275) is predicted to be an integral membrane protein comprised of 684 amino acids, where the N-terminal and C-terminal polypeptide segments relative to a single transmembrane helix are extracellular and cytoplasmic, respectively. In the NCBI RefSeq and UniProtKB<sup>[5]</sup> databases, CG2496 is annotated as a chromosome segregation ATPase, but there is currently no experimental evidence for this particular annotation. Homologous proteins are found in genomes of 43 other species of Corynebacteria. A significant portion of the N-terminal domain of CG2496 (residues 63–171) belongs to the TPM domain (named after proteins TLP18.3, Psb32 and MOLO-1) family (Pfam<sup>[6]</sup> accession: PF04536), which currently contains 3,085 protein sequences from 1,821 species, including bacteria, plants, protozoa and lower metazoa, such as nematodes and lancelets. Two TPM domain-containing proteins, TLP18.3 from *A. thaliana* and Psb32(SII1390) from

\*Corresponding author Fax: (402) 472-9402 rpowers3@unl.edu.

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*Synechocystis* sp., were shown to be involved in the photosystem II (PSII) repair cycle.<sup>[7]</sup> Phosphatase activity was reported for TLP18.3,<sup>[7b]</sup> however, the measured enzymatic activity levels were very low. In *C. elegans*, the TPM domain protein MOLO-1 acts as a modulator of the levamisole-sensitive acetylcholine receptor (L-AChR), but the function of TPM domain proteins in other organisms is still unknown. The Northeast Structural Genomics Consortium (NESG; <http://www.nesg.org>) recently determined the solution NMR structure<sup>[8]</sup> of the TPM domain of CG2496 comprising residues 41-180 (PDB ID: 2KPT; NESG target ID: CgR26A) which revealed a distinct architecture and provided the first structural representative for PF04536.

Here we describe the identification of low molecular weight compounds binding to the extracellular N-terminal domain of protein CG2496 from *C. glutamicum* using an NMR-based screening approach (FAST-NMR).<sup>[9]</sup> We expect that the newly identified compounds will also support future functional characterization of protein CG2496. Furthermore, assuming that protein CG2496 plays an important role for proliferation of *C. glutamicum*, we investigated to which extent one of the compounds, that is, methiothepin, inhibits cell growth.

1D <sup>1</sup>H NMR screening of the FAST-NMR library of 460 low molecular weight compounds resulted in 13 initial hits which showed broadening of <sup>1</sup>H NMR peaks in the presence of CG2496(41-180) (Table 1). Specific interaction with CG2496(41-180) was revealed by assessing chemical shift perturbations in 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC spectra recorded for CG2496(41-180) in the presence of each of the 13 compounds. Additionally, 5 more compounds from the library, which did not show line-broadening in the 1D <sup>1</sup>H NMR screen, were evaluated using the 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC screen. These compounds were selected to test hypotheses of CG2496(41-180) function. Of the 18 total compounds screened by 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC, 10 induced minor perturbations of a small number (<7) of 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC peaks. Only one compound, methiothepin, induced a significant number (~25) of chemical shift perturbations in the 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC spectrum of CG2496(41-180) (Figure 1). An NMR titration of CG2496(41-180) with methiothepin determined a dissociation constant ( $K_D$ ) of  $54 \pm 19 \mu\text{M}$ . Intriguingly, residues exhibiting significant chemical shift perturbations upon the binding of methiothepin are strongly conserved within the TPM domain family and are part of a mostly neutral and hydrophobic surface cleft (Figure 2), which was previously predicted as the putative active site.<sup>[8]</sup> Every compound that induced a chemical shift perturbation in the 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC showed a perturbation for Asp56, while 10 of 11 of these compounds showed perturbations for Tyr53. These two residues are also found in the predicted active site. Notably, methiothepin is a serotonin receptor antagonist commonly used as an United States food and drug administration (FDA) approved antipsychotic drug.<sup>[10]</sup>

Despite the available three-dimensional structure and similarity with TPM domains of known function, the function of the CG2496(41-180) domain remains unknown. Sequence similarity searches with BlastP<sup>[11]</sup> identify only uncharacterized proteins from Corynebacteria, while searches for structurally similar proteins with PDBeFold<sup>[12]</sup> and DALI<sup>[13]</sup> identify several phosphatases and the C-terminal domain of an alanyl-tRNA synthetase. However, our binding results did not indicate any interaction with typical phosphatase substrates, such as O-phospho-L-serine. The STRING<sup>[14]</sup> database indicates relationships with primarily hypothetical proteins, however a gene encoding a dGTP hydrolase and a gene encoding a histone N-acetyltransferase are loosely associated with CG2496(41-180). Furthermore, a comparison of the CG2496(41-180)-methiothepin binding site to a database of protein-ligand binding sites using CPASS<sup>[15]</sup> did not result in any hits above a 30% similarity threshold, which is the minimum score used to consider two proteins to have structurally and functionally similar binding sites.<sup>[15b]</sup>

Next, assuming that protein CG2496 plays an important role for *C. glutamicum*, we investigated if methiothepin inhibits cell growth. A disk diffusion assay (Figure 3) shows that methiothepin does indeed inhibit the growth of *C. glutamicum*. Additionally, a comparative minimum inhibitory concentration (MIC) test for methiothepin was performed for *C. glutamicum* and *S. aureus*, which does not possess a homolog of CG2496. *C. glutamicum* can only grow in media with up to 20 mM methiothepin. Conversely, *S. aureus* is able to grow at higher methiothepin concentrations of at least 40 mM. The low solubility of methiothepin in complex cell culture media prevented the use of higher concentrations and the determination of a reliable MIC value. However, the growth inhibition of *C. glutamicum* by methiothepin and the corresponding lack of activity against *S. aureus* suggests CG2496 is the *in vivo* target of methiothepin. Correspondingly, methiothepin would be expected to be active against other Corynebacteria containing a homolog of CG2496.

A tiered ligand-affinity screen using the FAST-NMR approach revealed that methiothepin, an FDA approved drug, binds to CG2496(41-180) and also inhibits the growth of *C. glutamicum*. The presence of CG2496 homologs in *Corynebacterium* spp. pathogens (e.g., the genomes of *C. ulcerans*, *C. diphtheriae*, and *C. pseudotuberculosis* encode homologs of CG2496 with 46%, 38%, and 43% sequence identity, respectively) suggests that methiothepin may bind to these proteins as well and may also act as an antibiotic for these species. These results identify the functionally uncharacterized CG2496 protein and its homologs as novel targets for drug discovery, and methiothepin as a potentially a lead compound to develop a new line of antibiotics against Corynebacteria.

## Experimental Section

Details of the FAST-NMR ligand affinity screens, the CG2496(41-180)-methiothepin NMR titration experiment, the generation of the of CG2496(41-180)-methiothepin complex structure, and the disk diffusion assay are provided in the Supporting Information.

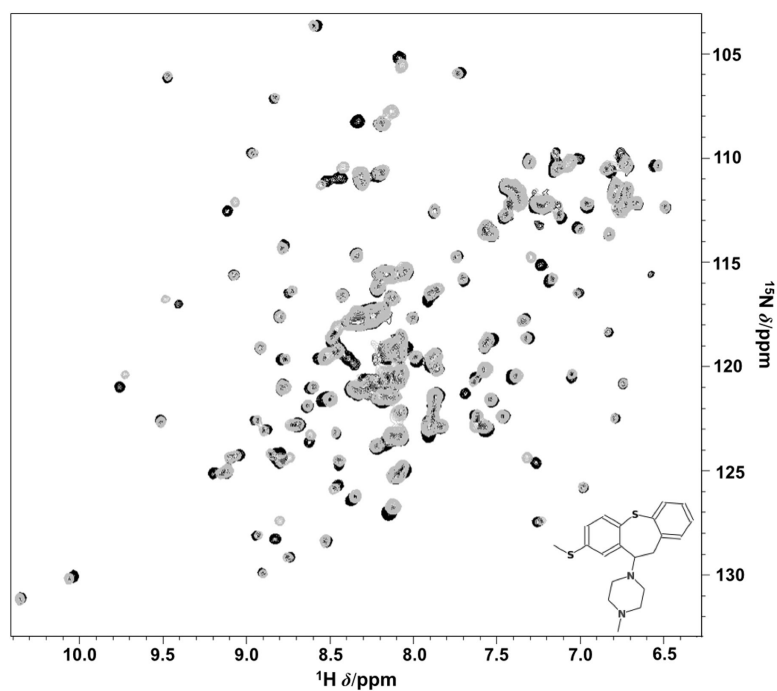
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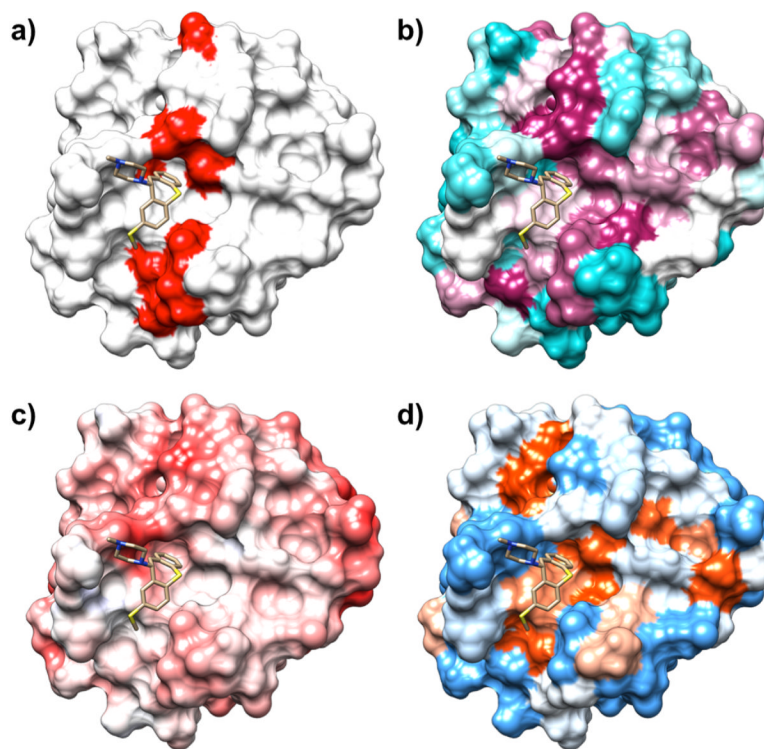
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**Figure 1.**

An overlay of 2D [ $^{15}\text{N}$ ,  $^1\text{H}$ ]-HSQC spectra of free CG2496(41-180) (black) and CG2496(41-180) bound with methiothepin (gray). The chemical structure of methiothepin is displayed in the lower right.

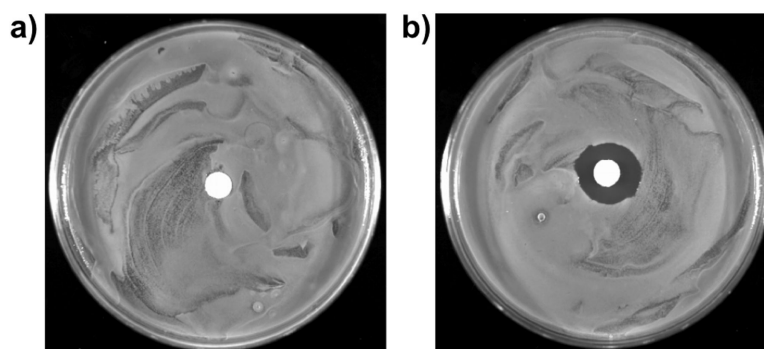




**Figure 2.**

a) The CG2496(41-180)-methiothepin complex generated by AutoDock where residues with significant chemical shift perturbations are colored red. b) ConSurf<sup>[16]</sup> residue conservation surface representation of the CG2496(41-180)-methiothepin complex where highly conserved residues are magenta and poorly conserved residues are cyan. c) UCSF Chimera<sup>[17]</sup> hydrophobicity surface representation of the CG2496(41-180)-methiothepin complex where the hydrophilic surface is blue and hydrophobic surface is orange. d) Delphi<sup>[18]</sup> electrostatics surface representation of the CG2496(41-180)-methiothepin complex where the positively-charged surface is blue and negatively-charged surface is red.





**Figure 3.**

Disk diffusion assay. *C. glutamicum* was plated and grown in the presence of a) a disk soaked with water and b) a disk soaked with an aqueous solution containing 400  $\mu$ M methiothepin.

**Table 1**

List of compounds from the FAST-NMR screen that bind CG2496(41-180)

Compound Name	1D Hits <sup>a</sup>	2D Hits <sup>b</sup>	Perturbed Residues <sup>c</sup>
N-succinyl-Ala-Ala-Pro-Phe p-nitroanilide	X	X	Y53, N56, V168
4-methylpyrazole	X	X	Y53, N56, V168
Bay 11-708	X	X	Y53, N56, V168
histamine	X	X	Y53, N56, V168
methiothepin	X	X	Y44, L46, Y53, N56, T58, G62, V79, V90, D96, T104, N111, G112, G114, V116
adenine	X	X	Y53, N56
1-methylimidazole	X	X	Y53, N56, V168
ethacridine	X	X	L46, Y53, N56, T58, F149, L162, V168
adenosine-5'-triphosphate <sup>d</sup>		X	N56, T58
serotonin <sup>d</sup>		X	Y53, N56, T58
adenosine-5'-monophosphate <sup>d</sup>		X	Y53, N56, V168

<sup>a</sup> Indicates compounds that exhibited line broadening in 1D <sup>1</sup>H NMR screen in the presence of CG2496(41-180)<sup>b</sup> Indicates compounds that caused peak perturbations in the 2D [<sup>1</sup>H, <sup>15</sup>N]-HSQC of CG2496(41-180)<sup>c</sup> Identity of the residues that were significantly perturbed (>1 standard deviation from mean perturbation) in the 2D [<sup>1</sup>H, <sup>15</sup>N]-HSQC of CG2496(41-180)<sup>d</sup> These compounds were evaluated in the 1D <sup>1</sup>H NMR screen but exhibited no line broadening. Evaluated in 2D [<sup>1</sup>H, <sup>15</sup>N]-HSQC screen to test potential CG2496(41-180) functions.

## Supporting Information

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### **Identification of Low-Molecular-Weight Compounds Inhibiting Growth of Corynebacteria: Potential Lead Compounds for Antibiotics**

Jaime L. Stark,<sup>[a]</sup> Jennifer C. Copeland,<sup>[a]</sup> Alexander Eletsy,<sup>[b]</sup> Greg A. Somerville,<sup>[c]</sup>  
Thomas Szyperski,<sup>[b]</sup> and Robert Powers<sup>\*[a]</sup>

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## Experimental Section

### *CG2496(41-180) samples*

Two samples of CG2496(41-180) were received from the Northeast Structural Genomics Consortium (NESG; <http://www.nesg.org>; NESG ID: CgR26A), where one sample was at natural abundance and the other was uniformly  $^{15}\text{N}$ -labeled. The structure of the protein was previously deposited in the RCSB PDB as 2KPT.<sup>[1]</sup> Amino acid chemical shift resonances for CG2496(41-180) were collected from the Biological Magnetic Resonance Data Bank (<http://www.bmrb.wisc.edu>).<sup>[2]</sup>

### *Function-based compound library and mixtures*

The compound library consists of functional ligands such as metabolites, substrates, inhibitors, and cofactors that have been shown to bind proteins and influence activity.<sup>[3]</sup> The compound library contains 460 active compounds that can be found in the BioScreen database (<http://bionmr.unl.edu/ligands>). Stock solutions for each compound are stored at  $-80\text{ }^{\circ}\text{C}$  in either dimethyl sulfoxide- $\text{d}_6$  or  $\text{D}_2\text{O}$  at a concentration of 20 mM. In order to minimize the number of NMR samples during the 1D line-broadening screen, the compounds are combined into 117 mixtures that consist of 3-4 compounds each, which has been determined to be the optimal 1D NMR mixture size.<sup>[4]</sup> The mixtures are created using equal volumes of individual compound stock solution, leading to a final concentration of 5 mM per ligand in each mixture.

### *NMR ligand-based screen*

The NMR samples for a 1D line-broadening screen were prepared in 10 mM  $\text{d}_{19}$ -bis-Tris

buffer at pH 6.5 in 99.99% D<sub>2</sub>O and 11.1 μM TMSP-d<sub>4</sub> to act as a chemical shift reference. Each sample had a 100 μM final concentration for each ligand in the mixture while the CG2496(41-180) protein (natural abundance) concentration was 10 μM. The 1D <sup>1</sup>H NMR spectra were collected on a Bruker 500 MHz Avance spectrometer with a triple-resonance, Z-axis gradient cryoprobe and BACS-120 sample changer using a 1D <sup>1</sup>H excitation sculpting pulse sequence to improve water suppression and signal-to-noise. The data was processed using ACD 1D NMR Processor. The spectra of the ligand mixtures with protein were visually compared to the spectra of the ligand mixtures without protein. A mixture was flagged as a potential binding event if the peak intensity of the protein-ligand sample decreased relative to the ligand-only sample.<sup>[5]</sup> The potential binding ligand was identified by comparing the broadened peak to reference spectra of ligands known to be in the mixture.

#### *NMR target-based screen*

For each compound that showed binding in the 1D line-broadening screen, an NMR sample of that compound in the presence of protein was prepared. The NMR sample consists of the ligand at 400 μM concentration and the CG2496(41-180) protein (<sup>15</sup>N-labeled) at 30 μM concentration in a 10 mM bis-Tris buffer at pH 6.5 and 10% D<sub>2</sub>O. The 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC experiments were collected on the same 500 MHz spectrometer described above using the WATERGATE and water flip-back pulses for solvent suppression. The data was processed using NMRPipe<sup>[6]</sup> and visualized in CCPNMR Analysis (<http://www.ccpn.ac.uk>). The resulting spectra were overlaid with the spectrum

of the free protein, and protein-ligand spectra that showed significant perturbations of NMR peaks relative to the free protein spectra were designated as binders.<sup>[7]</sup>

#### *Generation of CG2496(41-180)-methiothepin costructure*

The ligand (methiothepin) that caused the greatest magnitude chemical shift perturbations (CSPs) in the 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC screen was used to define the consensus binding site using in-house program CSP-Consensus. The three dimensional structures of both the ligand and the protein were prepared for docking (correcting for missing atoms) using UCSF Chimera.<sup>[8]</sup> AutoDock 4.2.3<sup>[9]</sup> with the AutoDockTools 1.5.4<sup>[9c, 10]</sup> (<http://mgltools.scripps.edu>) graphical interface was used to calculate 120 CG2496(41-180)-methiothepin costructures. The AutoDock grid was set to encompass the consensus-binding site identified from the in-house CSP-Consensus program with a grid spacing of 0.375 Å. The docking was performed using the Lamarckian genetic algorithm with a population of 300 and 2,500,000 energy evaluations. The docked structure that best agreed with the experimental CSPs from the 2D [<sup>15</sup>N,<sup>1</sup>H]-HSQC experiment was identified using in-house program AutoDockFilter 2.0.<sup>[11]</sup>

#### *NMR titration of CG2496(41-180) with methiothepin*

The titration analysis was performed with a 333 µM U-<sup>15</sup>N, 5%-<sup>13</sup>C-labeled CG2496(41-180) sample (5.7 mM MES buffer, pH 6.5 with 57 mM NaCl, 1.7 mM CaCl<sub>2</sub>, 0.007% NaN<sub>3</sub>, 3 mM DTT, 17 µM DSS, and 10% D<sub>2</sub>O) and six increasing concentrations of methiothepin (0 µM, 94.5 µM, 185.2 µM, 314.7 µM, 589.3 µM, and 1045.5 µM)

dissolved in the same buffer. The 2D [ $^{15}\text{N}$ ,  $^1\text{H}$ ]-HSQC experiments were collected on a Varian 600 MHz DD2 instrument equipped with a cryogenic probe. The data was processed using PROSA,<sup>[12]</sup> referenced to internal DSS, and visualized in CCPNMR Analysis (<http://www.ccpn.ac.uk>). The magnitude of the CSPs observed for each ligand concentration was used to determine the dissociation constant ( $K_D$ ) for the CG2496(41-180)-methiothepin complex using the following binding isotherm:<sup>[13]</sup>

$$\text{CSP}_{\text{obs}} = \text{CSP}_{\text{max}} \frac{(K_D + [L] + [P]) - \sqrt{(K_D + [L] + [P])^2 - (4[L][P])}}{2[P]} \quad (1)$$

where  $[P]$  is the protein concentration,  $[L]$  is the ligand concentration,  $\text{CSP}_{\text{max}}$  is the maximum chemical shift perturbation observed for a fully bound protein,  $\text{CSP}_{\text{obs}}$  is the observed chemical shift perturbation at each ligand concentration. A least squares fit of [Eq. (1)] to the normalized CSPs for ten perturbed amino acid residues (Glu51, Tyr53, Val90, Asp96, Thr104, Ala110, Asn111, Gly112, Gly113, Val116) was used to determine the average dissociation constant of methiothepin binding to CG2496(41-180).

#### *Disk diffusion assay*

The antimicrobial disk diffusion assay was performed by spreading  $\sim 10^5$  bacteria onto a Petri dish containing Mueller Hinton agar. After letting the Petri dish dry for 10 minutes, Whatman 3MM Chr paper disks (6 mm diameter) impregnated with 400  $\mu\text{M}$  methiothepin or water (negative control) were placed in the center of the Petri dishes. The Petri dishes were incubated for 12 hours at 37°C and photographed.



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